

SEQUENCE LISTING

<110> Dahlqvist, Andres
Stahl, Ulf
Lenman, Marit
Banas, Antoni
Ronne, Hans

<120> A new class of enzymes in the biosynthetic pathway for the production of triacylglycerol and recombinant DNA molecules encoding these enzymes

<130> BASFnae337799PCT1-15

<140> US 09/537,710

<141> 2000-03-30

<150> EP 99106656.4

<151> 1999-04-01

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8'
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B1
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B'
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 Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
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 65 70 75 80
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 115 120 125
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 165 170 175
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 Val Leu Ile Ala Asn Leu Ala His Ile Gly Tyr Glu Glu Lys Asn Met
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 Arg Asp Gln Thr Leu Ser Arg Met Lys Ser Asn Ile Glu Leu Met Val

B'
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Leu Gly Gly Gly Gly Gly Gly Pro Asp Trp Cys Ala Lys Tyr Ile Lys Ala						
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Val Met Asn Ile Gly Gly Pro Phe Leu Gly Val Pro Lys Ala Val Ala						
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Gly Leu Phe Ser Ala Glu Ala Lys Asp Val Ala Val Ala Arg Ala Ile						
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Ala Pro Gly Phe Leu Asp Thr Asp Ile Phe Arg Leu Gln Thr Leu Gln						
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His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu						
	340			345		350
Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu						
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Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys						
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	385			390		395
Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser						
	405			410		415
Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile						
	420			425		430
Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly						
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Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly						
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Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr						
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Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu						
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B'
cont.

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Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
595 600 605

His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
610 615 620

Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
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Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
20 25 30
tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
35 40 45
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Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
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acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240

B!
cont.

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 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
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 <213> Zea mays

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 35 40 45
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
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<213> Neurospora crassa

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<213> Arabidopsis thaliana

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<212> DNA

<213> Arabidopsis thaliana

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B'
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 <211> 623
 <212> PRT
 <213> *Schizosaccharomyces pombe*

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 Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
 50 55 60
 Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala
 65 70 75 80

Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
 85 90 95
 Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
 100 105 110
 Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
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 Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser
 130 135 140
 Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
 145 150 155 160
 Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
 165 170 175
 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
 180 185 190
 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
 195 200 205
 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
 210 215 220
 Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala
 225 230 235 240
 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
 245 250 255
 Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
 260 265 270
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
 275 280 285
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
 290 295 300
 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
 305 310 315 320
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
 325 330 335
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
 340 345 350
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
 355 360 365
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro

B'
 int.

370

375

380

Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
385 390 395 400

Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
405 410 415

Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
420 425 430

Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
435 440 445

Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
450 455 460

Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
465 470 475 480

Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
485 490 495

Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
500 505 510

Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
515 520 525

Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
530 535 540

Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
610 615 620

<210> 14

<211> 432

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val

1	5	10	15
Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr	20	25	30
Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg	35	40	45
Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu	50	55	60
Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp	65	70	75
Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met	85	90	95
Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly	100	105	110
Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr	115	120	125
Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val	130	135	140
Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu	145	150	155
Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro	165	170	175
Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu	180	185	190
Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His	195	200	205
Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro	210	215	220
Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro	225	230	235
Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr	245	250	255
Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg	260	265	270
Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His	275	280	285
Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala	290	295	300

B'
int.

Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
 305 310 315 320
 Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
 325 330 335
 Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
 340 345 350
 Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
 355 360 365
 Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
 370 375 380
 Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
 385 390 395 400
 Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
 405 410 415
 Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
 420 425 430

B¹
 cont.
 <210> 15
 <211> 552
 <212> PRT
 <213> Arabidopsis thaliana

<400> 15
 Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala
 1 5 10 15
 Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr
 20 25 30
 Glu Phe His Gly Asp Tyr Ser Lys Leu Ser Gly Ile Ile Ile Pro Gly
 35 40 45
 Phe Ala Ser Thr Gln Leu Arg Ala Trp Ser Ile Leu Asp Cys Pro Tyr
 50 55 60
 Thr Pro Leu Asp Phe Asn Pro Leu Asp Leu Val Trp Leu Asp Thr Thr
 65 70 75 80
 Lys Leu Leu Ser Ala Val Asn Cys Trp Phe Lys Cys Met Val Leu Asp
 85 90 95
 Pro Tyr Asn Gln Thr Asp His Pro Glu Cys Lys Ser Arg Pro Asp Ser
 100 105 110

Gly Leu Ser Ala Ile Thr Glu Leu Asp Pro Gly Tyr Ile Thr Gly Pro
 115 120 125
 Leu Ser Thr Val Trp Lys Glu Trp Leu Lys Trp Cys Val Glu Phe Gly
 130 135 140
 Ile Glu Ala Asn Ala Ile Val Ala Val Pro Tyr Asp Trp Arg Leu Ser
 145 150 155 160
 Pro Thr Lys Leu Glu Glu Arg Asp Leu Tyr Phe His Lys Leu Lys Leu
 165 170 175
 Thr Phe Glu Thr Ala Leu Lys Leu Arg Gly Gly Pro Ser Ile Val Phe
 180 185 190
 Ala His Ser Met Gly Asn Asn Val Phe Arg Tyr Phe Leu Glu Trp Leu
 195 200 205
 Arg Leu Glu Ile Ala Pro Lys His Tyr Leu Lys Trp Leu Asp Gln His
 210 215 220
 Ile His Ala Tyr Phe Ala Val Gly Ala Pro Leu Leu Gly Ser Val Glu
 225 230 235 240
 Ala Ile Lys Ser Thr Leu Ser Gly Val Thr Phe Gly Leu Pro Val Ser
 245 250 255
 Glu Gly Thr Ala Arg Leu Leu Ser Asn Ser Phe Ala Ser Ser Leu Trp
 260 265 270
 Leu Met Pro Phe Ser Lys Asn Cys Lys Gly Asp Asn Thr Phe Trp Thr
 275 280 285
 His Phe Ser Gly Gly Ala Ala Lys Lys Asp Lys Arg Val Tyr His Cys
 290 295 300
 Asp Glu Glu Glu Tyr Gln Ser Lys Tyr Ser Gly Trp Pro Thr Asn Ile
 305 310 315 320
 Ile Asn Ile Glu Ile Pro Ser Thr Ser Ala Arg Glu Leu Ala Asp Gly
 325 330 335
 Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met
 340 345 350
 Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile
 355 360 365
 Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro
 370 375 380
 Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val
 385 390 395 400
 Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe

B'
 unA

405 410 415
 Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile
 420 425 430
 Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val
 435 440 445
 Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His
 450 455 460
 Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr
 465 470 475 480
 Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His
 485 490 495
 Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly
 500 505 510
 Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile
 515 520 525
 Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val
 530 535 540
 Trp Glu Leu Asp Lys Ser Gly Tyr
 545 550

<210> 1a
 <211> 661
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 1a
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe

100							105					110				
Val	Asn	Phe	Asp	Ser	Leu	Lys	Val	Tyr	Leu	Asp	Asp	Trp	Lys	Asp	Val	
115							120						125			
Leu	Pro	Gln	Gly	Ile	Ser	Ser	Phe	Ile	Asp	Asp	Ile	Gln	Ala	Gly	Asn	
130							135						140			
Tyr	Ser	Thr	Ser	Ser	Leu	Asp	Asp	Leu	Ser	Glu	Asn	Phe	Ala	Val	Gly	
145							150						155			
Lys	Gln	Leu	Leu	Arg	Asp	Tyr	Asn	Ile	Glu	Ala	Lys	His	Pro	Val	Val	
			165							170			175			
Met	Val	Pro	Gly	Val	Ile	Ser	Thr	Gly	Ile	Glu	Ser	Trp	Gly	Val	Ile	
			180							185			190			
Gly	Asp	Asp	Glu	Cys	Asp	Ser	Ser	Ala	His	Phe	Arg	Lys	Arg	Leu	Trp	
			195							200			205			
Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp	
210							215						220			
Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn	
225							230						235			
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile	
			245							250			255			
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile	
			260							265			270			
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu	
275							280						285			
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys	
290							295						300			
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu	
305							310						315			
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp	
			325							330			335			
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val	
			340							345			350			
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly	
			355							360			365			
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr	
370							375						380			
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser	
385							390						395			
													400			

B'
int.

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 2a
 <211> 387
 <212> PRT

<213> Arabidopsis thaliana

<400> 2a

Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro Gly Asn Gly Gly
1 5 10 15

Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val
20 25 30

Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp
35 40 45

Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg
50 55 60

Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp
65 70 75 80

Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser
85 90 95

Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser
100 105 110

Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val
115 120 125

Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu
130 135 140

Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp
145 150 155 160

Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro
165 170 175

Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe
180 185 190

Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe
195 200 205

Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr
210 215 220

Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu
225 230 235 240

Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
245 250 255

Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
260 265 270

Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile

B'
cont.

275 280 285
 Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
 290 295 300
 Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
 305 310 315 320
 Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe
 325 330 335
 Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
 340 345 350
 Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
 355 360 365
 Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
 370 375 380
 Lys Glu Ile
 385

B'
 uny.
 <210> 3a
 <211> 389
 <212> PRT
 <213> Arabidopsis thaliana

<400> 3a
 Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
 1 5 10 15
 Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
 20 25 30
 Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
 35 40 45
 Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
 50 55 60
 Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
 65 70 75 80
 Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
 85 90 95
 Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
 100 105 110
 Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
 115 120 125
 Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile

130 135 140
 Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
 145 150 155 160
 Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys
 165 170 175
 Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
 180 185 190
 Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
 195 200 205
 Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
 210 215 220
 Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
 225 230 235 240
 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
 245 250 255
 Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
 260 265 270
 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
 275 280 285
 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
 290 295 300
 Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
 305 310 315 320
 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
 325 330 335
 Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
 340 345 350
 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
 355 360 365
 Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
 370 375 380
 Gly Ile Phe Glu Trp
 385

B'
 cont.

<210> 4a
 <211> 1986
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1983)

<400> 4a

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
1 5 10 15

gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80

B' cont.
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
115 120 125

ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
130 135 140

tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
145 150 155 160

aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
165 170 175

atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
180 185 190

gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp

195	200	205	
gga agt ttt tac atg ctg	aga aca atg gtt atg gat	aaa gtt tgt tgg	672
Gly Ser Phe Tyr Met Leu	Arg Thr Met Val Met Asp	Lys Val Cys Trp	
210	215	220	
ttg aaa cat gta atg tta gat	cct gaa aca ggt ctg gac	cca ccg aac	720
Leu Lys His Val Met Leu	Asp Pro Glu Thr Gly Leu	Asp Pro Pro Asn	
225	230	235 240	
ttt acg cta cgt gca gca	cag ggc ttc gaa tca act	gat tat ttc atc	768
Phe Thr Leu Arg Ala Ala	Gln Gly Phe Glu Ser Thr	Asp Tyr Phe Ile	
245	250	255	
gca ggg tat tgg att tgg	aac aaa gtt ttc caa aat	ctg gga gta att	816
Ala Gly Tyr Trp Ile Trp	Asn Lys Val Phe Gln Asn	Leu Gly Val Ile	
260	265	270	
ggc tat gaa ccc aat aaa	atg acg agt gct gcg tat	gat tgg agg ctt	864
Gly Tyr Glu Pro Asn Lys	Met Thr Ser Ala Ala Tyr	Asp Trp Arg Leu	
275	280	285	
gca tat tta gat cta gaa	aga cgc gat agg tac ttt	acg aag cta aag	912
Ala Tyr Leu Asp Leu Glu	Arg Arg Asp Arg Tyr Phe	Thr Lys Leu Lys	
290	295	300	
gaa caa atc gaa ctg ttt	cat caa ttg agt ggt gaa	aaa gtt tgt tta	960
Glu Gln Ile Glu Leu Phe	His Gln Leu Ser Gly Glu	Lys Val Cys Leu	
305	310	315 320	
att gga cat tct atg ggt	tct cag att atc ttt tac	ttt atg aaa tgg	1008
Ile Gly His Ser Met Gly	Ser Gln Ile Ile Phe Tyr	Phe Met Lys Trp	
325	330	335	
gtc gag gct gaa ggc cct	ctt tac ggt aat ggt ggt	cgt ggc tgg gtt	1056
Val Glu Ala Glu Gly Pro	Leu Tyr Gly Asn Gly Gly	Arg Gly Trp Val	
340	345	350	
aac gaa cac ata gat tca	ttc att aat gca gca ggg	acg ctt ctg ggc	1104
Asn Glu His Ile Asp Ser	Phe Ile Asn Ala Ala Gly	Thr Leu Leu Gly	
355	360	365	
gct cca aag gca gtt cca	gct cta att agt ggt gaa	atg aaa gat acc	1152
Ala Pro Lys Ala Val Pro	Ala Leu Ile Ser Gly Glu	Met Lys Asp Thr	
370	375	380	
att caa tta aat acg tta	gcc atg tat ggt ttg gaa	aag ttc ttc tca	1200
Ile Gln Leu Asn Thr Leu	Ala Met Tyr Gly Leu Glu	Lys Phe Phe Ser	
385	390	395 400	
aga att gag aga gta aaa	atg tta caa acg tgg ggt	ggt ata cca tca	1248
Arg Ile Glu Arg Val Lys	Met Leu Gln Thr Trp Gly	Gly Ile Pro Ser	
405	410	415	
atg cta cca aag gga gaa	gag gtc att tgg ggg gat	atg aag tca tct	1296

B¹
wt.

Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser	
			420					425					430			
tca	gag	gat	gca	ttg	aat	aac	aac	act	gac	aca	tac	ggc	aat	ttc	att	1344
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile	
			435				440					445				
cga	ttt	gaa	agg	aat	acg	agc	gat	gct	ttc	aac	aaa	aat	ttg	aca	atg	1392
Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met	
			450				455				460					
aaa	gac	gcc	att	aac	atg	aca	tta	tcg	ata	tca	cct	gaa	tgg	ctc	caa	1440
Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln	
465						470				475					480	
aga	aga	gta	cat	gag	cag	tac	tcg	ttc	ggc	tat	tcc	aag	aat	gaa	gaa	1488
Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu	
			485						490					495		
gag	tta	aga	aaa	aat	gag	cta	cac	cac	aag	cac	tgg	tcg	aat	cca	atg	1536
Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met	
			500					505					510			
gaa	gta	cca	ctt	cca	gaa	gct	ccc	cac	atg	aaa	atc	tat	tgt	ata	tac	1584
Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr	
			515				520					525				
ggg	gtg	aac	aac	cca	act	gaa	agg	gca	tat	gta	tat	aag	gaa	gag	gat	1632
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp	
			530				535				540					
gac	tcc	tct	gct	ctg	aat	ttg	acc	atc	gac	tac	gaa	agc	aag	caa	cct	1680
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro	
545						550				555					560	
gta	ttc	ctc	acc	gag	ggg	gac	gga	acc	gtt	ccg	ctc	gtg	gcg	cat	tca	1728
Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser	
				565				570						575		
atg	tgt	cac	aaa	tgg	gcc	cag	ggt	gct	tca	ccg	tac	aac	cct	gcc	gga	1776
Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly	
			580				585						590			
att	aac	gtt	act	att	gtg	gaa	atg	aaa	cac	cag	cca	gat	cga	ttt	gat	1824
Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp	
			595				600					605				
ata	cgt	ggt	gga	gca	aaa	agc	gcc	gaa	cac	gta	gac	atc	ctc	ggc	agc	1872
Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser	
			610				615				620					
gcg	gag	ttg	aac	gat	tac	atc	ttg	aaa	att	gca	agc	ggt	aat	ggc	gat	1920
Ala	Glu	Leu	Asn	Asp	Tyr	Ile	Leu	Lys	Ile	Ala	Ser	Gly	Asn	Gly	Asp	
625						630				635					640	

B'
cont.

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag	1968
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln	
645 650 655	

atg ccc ttc cca atg taa	1986
Met Pro Phe Pro Met	
660	

<210> 5a
 <211> 661
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 5a
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
85 90 95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
130 135 140

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
195 200 205

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp

B'
 cont.

210	215	220
Leu Lys His Val Met	Leu Asp Pro Glu Thr Gly	Leu Asp Pro Pro Asn
225	230	235 240
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile		
	245	250 255
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile		
	260	265 270
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu		
	275	280 285
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys		
	290	295 300
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu		
	305	310 315 320
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp		
	325	330 335
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val		
	340	345 350
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly		
	355	360 365
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr		
	370	375 380
Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser		
	385	390 395 400
Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser		
	405	410 415
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser		
	420	425 430
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile		
	435	440 445
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met		
	450	455 460
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln		
	465	470 475 480
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu		
	485	490 495
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met		
	500	505 510

B'
cont.

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
645 650 655

Met Pro Phe Pro Met
660

<210> 1b
<211> 1986
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(1983)

<400> 1b
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Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
1 5 10 15
gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
20 25 30
aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
35 40 45
att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg	240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
65 70 75 80	
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt	288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
85 90 95	
ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	
100 105 110	
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val	
115 120 125	
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn	
130 135 140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly	
145 150 155 160	
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val	
165 170 175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile	
180 185 190	
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp	
195 200 205	
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp	
210 215 220	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn	
225 230 235 240	
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile	
245 250 255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile	
260 265 270	
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu	
275 280 285	

B1
cont.

gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys	
290 295 300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu	
305 310 315 320	
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp	
325 330 335	
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val	
340 345 350	
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc	1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	
355 360 365	
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc	1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	
370 375 380	
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca	1200
Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	
385 390 395 400	
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca	1248
Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser	
405 410 415	
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct	1296
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser	
420 425 430	
tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att	1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile	
435 440 445	
cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg	1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met	
450 455 460	
aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa	1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln	
465 470 475 480	
aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa	1488
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu	
485 490 495	
gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg	1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met	
500 505 510	

B'
cont.

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 2b
 <211> 661
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 2b
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

B'
 cont.

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val

B1
cont.

340										345					350				
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly				
		355					360					365							
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr				
	370					375					380								
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser				
385					390					395					400				
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser				
			405						410					415					
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser				
		420						425					430						
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile				
	435						440					445							
Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met				
	450					455					460								
Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln				
465					470					475					480				
Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu				
			485						490					495					
Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met				
		500						505					510						
Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr				
	515						520					525							
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp				
	530					535					540								
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro				
545					550					555					560				
Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser				
			565					570						575					
Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly				
		580						585					590						
Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp				
	595						600						605						
Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser				
	610					615					620								
Ala	Glu	Leu	Asn	Asp	Tyr	Ile	Leu	Lys	Ile	Ala	Ser	Gly	Asn	Gly	Asp				
625					630					635					640				

B'
cont.

Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
645 650 655

Met Pro Phe Pro Met
660

<210> 3b
<211> 2312
<212> DNA
<213> Schizosaccharomyces pombe

<400> 3b
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gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccttc agcgtccgaa 120
acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
ttgggcgcta ttttggaat atgcggtgct ttttttttcg ctggttgaga cgacaatgct 240
gttttcgacc ctgctacgtt agataaattt gggaatatgc taggctcttc agacttggtt 300
gatgacatta aaggatattt atcttataat gtgtttaagg atgcaccttc tactacggac 360
aagccttcgc agtctcctag cggaaatgaa gttcaagttg gtcttgatat gtacaatgag 420
ggatatcgaa gtgaccatcc tgttattatg gttcctggtg ttatcagctc aggattagaa 480
agttggctcg ttaataattg ctcgattcct tacttttagga aacgtctttg gggtagctgg 540
tctatgctga aggcaatggt ccttgacaag caatgctggc ttgaacattt aatgcttgat 600
aaaaaaaccg gcttgatcc gaagggaatt aagctgcgag cagctcaggg gtttgaagca 660
gctgattttt ttatcacggg ctattggatt tggagtaaag taattgaaaa ccttgctgca 720
atttggttat agcctaataa catgttaagt gcttcttacg attggcgggt atcatatgca 780
aatttagagg aacgtgataa atatttttca aagttaaaaa tgttcattga gtacagcaac 840
attgtacata agaaaaaggt agtgttgatt tctcactcca tgggttcaca gggtacgtac 900
tattttttta agtgggttga agctgagggc tacggaaatg gtggaccgac ttgggttaac 960
gatcatattg aagcatttat aaatgtgagt ctcgatgggt gtttgactac gtttctaact 1020
tttgaataga tatcgggatc tttgattgga gcacccaaaa cagtggcagc gcttttatcg 1080
ggtgaaatga aagatacagg tattgtaatt acattaaaca tgttaatat taatttttgc 1140
taaccgtttt aagctcaatt gaatcagttt tcgggtctat ggtaagcaat aaattgttga 1200
gatttggttac taatttactg tttagtttgg aaaaattttt ttcccgttct gaggtatatt 1260
caaaaataca aatgtgctct actttttcta acttttaata gagagccatg atggttcgca 1320
ctatgggagg agttagttct atgcttccta aaggaggcga tgttgatagg ggaaatgcca 1380
gttggtgtaag aaatatgtgc tgttaatttt ttattaatat ttaggctcca gatgatctta 1440
atcaaacaaa tttttccaat ggtgcaatta ttcgatatag agaagacatt gataaggacc 1500
acgatgaatt tgacatagat gatgcattac aattttttaa aaatgttaca gatgacgatt 1560
ttaaagtcac gctagcgaaa aattattccc acggtcttgc ttggactgaa aaagaagtgt 1620
taaaaaataa cgaaatgccg tctaaatgga taaatccgct agaagtaaga acattaaagt 1680
tactaaatta tactaaccce aatagactag tcttccttat gctcctgata tgaaaattta 1740
ttgcgttcac ggggtcggaa aaccaactga gagaggttat tattatacta ataactctga 1800
ggggcaacct gtcattgatt cctcgggtta tgatggaaca aaagttgaaa atgtgagaga 1860
atztatgttt caaacattct attaaactgt ttattagggt attgttatgg atgatggtga 1920
tggaacttta ccaatattag cccttggttt ggtgtgcaat aaagtttggc aaacaaaaag 1980
gtttaatcct gctaatacaa gtatcacaaa ttatgaaatc aagcatgaac ctgctgcgtt 2040
tgatctgaga ggaggacctc gctcggcaga acacgtcgat atacttggac attcagagct 2100
aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aaggaaatta 2160
ttttaaaagt ttcacagggc catggtgact cggtagcaaa ccgttatata tcagatatcc 2220
agtacggaca taagttttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
atgagataaa tctcgataaa cctagaattt aa 2312

B'
cont.

<210> 4b
<211> 3685
<212> DNA
<213> Arabidopsis thaliana

<400> 4b

atgccccctta ttcacgcgaa aaagccgacg gagaaacat cgacgccgcc atctgaagag 60
gtggtgcacg atgaggattc gcaaaagaaa ccacacgaat cttccaaatc ccaccataag 120
aaatcgaacg gaggaggga ggtgctgtgc atcgattctt gttggtggtt cattgggtgt 180
gtgtgtgtaa cctggtggtt tcttctcttc ctttacaacg caatgcctgc gagcttcctt 240
cagtatgtaa cggagcgaat cacgggtcct ttgcctgacc cgcccgggtg taagctcaaa 300
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